

Amendment D
U.S. Appl. 09/490,609
May 25, 2004

Amendments to the Claims

The following listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims

1-24. (canceled).

25. (Currently amended) A method for determining a level or pattern of a carcinogenesis biomarker in a cell *in vitro* comprising:

(a) incubating, under conditions permitting specific nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ NOS: 280 and 488 or complements thereof, with a nucleic acid molecule obtained from said cell, wherein nucleic acid hybridization between said marker nucleic acid molecule, and said complementary nucleic acid molecule obtained from said cell permits the detection of said carcinogenesis biomarker;

(b) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said cell; and

(c) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said carcinogenesis biomarker.

26. (Original) The method of claim 25, wherein said level is predictive of said carcinogenesis biomarker.

27. (Original) The method of claim 25, wherein said pattern is predictive of said carcinogenesis biomarker.

28. (Original) The method of claim 25, wherein said level or pattern is detected by *in situ* hybridization.

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31. (Currently amended) A method for measuring the carcinogenicity of a composition comprising:

- (a) [(i.)] culturing a cell line in vitro;
- (b) [(ii.)] exposing said cell line to said composition; and
- (c) [(iii.)] determining the presence or absence of mRNA which substantially hybridizes to at least one nucleic acid sequence selected from the group consisting of SEQ NOS: 280, 384, and 488 and complements thereof.

32. (Currently Amended) A method for measuring the carcinogenicity of a composition comprising:

- (a) [(a.)] exposing a hepatocyte in vitro to said composition; and
- (b) [(b.)] detecting the presence or absence in said hepatocyte of mRNA which substantially hybridizes to [(an)] at least one nucleic acid sequence selected from the group consisting of SEQ NOS: 280, 384, and 488 and complements thereof.

33. (Original) The method of claim 32; wherein said hepatocyte is a rat hepatocyte.